

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/540,047

Source:

PT/10

Date Processed by STIC:

6/30/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

BEST AVAILABLE COPY

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/540,047</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input checked="" type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid.	

BEST AVAILABLE COPY



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/540,047

DATE: 06/30/2005
TIME: 09:05:27

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\06302005\J540047.raw

```

3 <110> APPLICANT: FUNDACION PARA LA INVESTIGACION CLINICA Y MOLECULAR
4   DEL CANCER DE PULMON (LUNG CANCER CLINICAL AND MOLECULAR
5   RESEARCH FOUNDATION)
W--> 6 <120> TITLE OF INVENTION: "ASSAY DEVICE OF XPD/ERCC2 GENE POLYMORPHISMS FOR THE
W--> 7   CORRECT ADMINISTRATION OF CHEMOTHERAPY IN LUNG CANCER"
W--> 8 <130> FILE REFERENCE: PCT-152
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/540,047
C--> 9 <141> CURRENT FILING DATE: 2005-06-22
W--> 9 <160> NUMBER OF SEQ ID: 8

```

*see item 4 on
Error summary sheet*

ERRORED SEQUENCES

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E--> 10 <210> SEQ ID NO: SEQ ID NO.:1
11 <211> LENGTH: 15
E--> 12 <212> TYPE: oligonucleotide
13 <213> ORGANISM: artificial sequence
W--> 14 <220> FEATURE:
W--> 15 <221> NAME/KEY: primer
W--> 16 <223> OTHER INFORMATION:
W--> 16 <400> SEQUENCE:
17 acgcccaccc ggccta      15
E--> 19 <210> SEQ ID NO: SEQ ID NO.: 2
20 <211> LENGTH: 17
E--> 21 <212> TYPE: oligonucleotide
22 <213> ORGANISM: artificial sequence
W--> 23 <220> FEATURE:
W--> 24 <221> NAME/KEY: primer
W--> 25 <223> OTHER INFORMATION:
W--> 25 <400> SEQUENCE:
26 ggcgggaaag ggactgg      17
E--> 28 <210> SEQ ID NO: SEQ ID NO.: 3
29 <211> LENGTH: 19
E--> 30 <212> TYPE: oligonucleotide
31 <213> ORGANISM: artificial sequence
W--> 32 <220> FEATURE:
W--> 33 <221> NAME/KEY: primer
34 <223> OTHER INFORMATION: TaqMan MGBTM VIC Probe
W--> 35 <400> SEQUENCE:
36 ccgtgctgcc cgacgaagt      19
E--> 38 <210> SEQ ID NO: SEQ ID NO.: 4
39 <211> LENGTH: 19
E--> 40 <212> TYPE: oligonucleotide

```

*Does Not Comply
Corrected Diskette Needed*

*See attached
pages for error
explanations.*

*Suggestion: consult
Sequence Rules
for valid format*

replace with
SEQUENCE LISTING (do not
print)

10/540,047

LIST OF SEQUENCES

do NOT include foreign accent marks. They cannot be processed.

<110> FUNDACION PARA LA INVESTIGACION CLINICA Y MOLECULAR

DEL CANCER DE PULMON (LUNG CANCER CLINICAL AND MOLECULAR
RESEARCH FOUNDATION)

<120> "ASSAY DEVICE OF XPD/ERCC2 GENE POLYMORPHISMS FOR THE
CORRECT ADMINISTRATION OF CHEMOTHERAPY IN LUNG CANCER"

<130> PCT-152

<160> 8 *delete all alphabetical headers*

<210> SEQ ID NO. 1

<211> 15

<212> oligonucleotide

<213> artificial sequence

<220>

<223> <221> primer

<400> 1<- insert

acgccccaccc ggcca

invited response.

*The only valid
responses are: DNA,
RNA or PRT. For a
combined DNA/RNA
sequence, use <212> DNA
and explain in
section.*

*do
NOT
use
ITALICS.
Use a
fixed-width
font, per
1.824 of
Sequence
Rules*

*replace
with*
↓
*explanation
for*

*Artificial Sequence
goes on
<223> line*

<210> SEQ ID NO. 2

<211> 17

<212> oligonucleotide

<213> artificial sequence

<220>

<221> primer

<400> 2 <

ggcgggaaag ggactgg

17

<210> SEQ ID NO. 3

<211> 19

<212> oligonucleotide

<213> artificial sequence

<220>

<221> primer *move up*

<223> (TaqMan MGBTM) VIC Probe

delete

<400> 3 ←

ccgtgctgcc cgacgaagt

19

<210> ~~SEQ ID NO.~~ 4

<211> 19

<212> oligonucleotide

<213> artificial sequence

<220>

<221> primer

<223> TaqMan MGB™ 6-FAM Probe

<400> 4 ←

cccggtgctgc ccaacgaag

19

<210> ~~SEQ ID NO.~~ 5

<211> 22

<212> oligonucleotide

<213> artificial sequence

<220>

<221> primer

<400> 5 ←

gcctggagca gcttagaatca ga

22

<210> ~~SEQ ID NO.~~ 6

<211> 22

<212> oligonucleotide

<213> artificial sequence

<220>

<221> primer

<400> 6 ←

cactcagacgc tgctgagcaa tc

22

<210> ~~SEQ ID NO.~~ 7

<211> 16

<212> oligonucleotide

10/540,047 4

<213> artificial sequence
<220>
<221> primer
~~<223> TaqMan MGB™ VIC Probe~~

<400> 7 ←

tatcctctgc agcgtc

16

<210> SEQ_ID_NO. 8

<211> 17

<212> oligonucleotide

<213> artificial sequence

<220>

<223> <221> primer

~~<223> TaqMan MGB™ 6-FAM Probe~~

<400> 8 ←

catacctttt cagcgtc

17